



Figure S1 A comparison between mutational signature analysis using the MAF data from TCGA database. A hypothetical MAF data was estimated by extracting 415 genes (identical to the CANCERPLEX gene panel) from the WES data. Although the percentages of each signature were different, three signatures, SI4 (etiology: exposure to tobacco mutagens), SI7 (etiology: UV exposure), and SI13 (etiology: APOBEC Cytidine Deaminase), were selected based on cosine-similarity, either from the WES data (A) or from the hypothetical data (B) (Maftools, R version 0.9.30). MAF, Mutation Annotation Format; TCGA, The Cancer Genome Atlas; WES, whole exome sequencing; SI, signature; UV, ultraviolet; APOBEC, apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like.